

Mahmoud Ahmed

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SUMMARY

I use public high-throughput data to learn about the process of autophagy. I build open source tools for managing data in my lab, mainly R packages, and shiny applications.

EDUCATION

Gyeongsang National University

Graduate school

Master's & PhD

Grad. Feb. 2018 & 2021

Cairo University

Kasr-alainy School of Medicine

Bachelor of Medicine and surgery

Grad. May 2015

SKILLS

Workflows:

Genomic data processing,

Network analysis

Programming:

R, Python

Tools:

UNIX, docker, Git, LaTeX

Languages:

Arabic (native), English

CERTIFICATES

Coursera Specializations:

Mastering Software Development in R,

Genomic Data Science,

Data Science,

Academic English: Writing

edX Programs:

Data Analysis for the Life Sciences,

Genomics Data Analysis

VOLUNTEERING

Staff member and outdoors activity instructor for youth and scout activity centers.

Gilwell Park

London, UK

SAPSC

Suncheon, SK

Camp Lakota

Ohio, USA

04.04.2021

RESEARCH

Gyeongsang National University

Graduate Student & Postdoc

2016 – present

Jinju, South Korea

- Investigating the role of the autophagy in the development and differentiation of fat cells
- Studying the regulation of gene expression by genetic and epigenetic means
- Building tools for managing and analyzing data

PUBLICATIONS

- Mahmoud Ahmed, Do Sik Min and Deok Ryong Kim. "Integrating binding and expression data to predict transcription factors combined function". In: BMC Genomics 21.1 (Dec. 2020), p. 610
- Mahmoud Ahmed and Deok Ryong Kim. "Modelling the gene expression and the DNA-binding in the 3T3-L1 differentiating adipocytes." In: Adipocyte 8.1 (Dec. 2019), pp. 401–411
- Mahmoud Ahmed et al. "Functional Linkage of RKIP to the Epithelial to Mesenchymal Transition and Autophagy during the Development of Prostate Cancer". In: Cancers 10.8 (Aug. 2018), p. 273

OPEN SOURCE

- target: An R Package to Predict Combined Function of Transcription Factors
- colocr: An R package for conducting co-localization analysis in fluorescence microscopy images.
- pcr: Quality assessing, analyzing and testing the statistical significance of real-time quantitative PCR data.
- cRegulome: An R package to access, manage and visualize regulome-gene correlations in cancer.
- miRCancerdb: A database for microRNA-gene/protein expression correlation in cancer.

TASK PREFERENCE

- ☆☆☆ Writing code to get and clean data
- ☆☆☆ Performing and reproducing an analysis
- ☆☆☆ Visualizing and presenting findings
- ☆☆☆ Writing a manuscript to be reviewed by strangers
- ☆☆☆ Arguing with the strangers